



SEQUENCE LISTING

<110> LEDBETTER, JEFFREY
HAYDEN-LEDBETTER, MARTHA

<120> DNA VACCINES ENCODING ANTIGEN LINKED TO A DOMAIN THAT BINDS CD40

<130> 034474.0003 UTL1

<140> 09/687,864
<141> 2000-10-13

<150> US 60/159,690
<151> 1999-10-14

<160> 29

<170> PatentIn Ver. 3.2

<210> 1
<211> 66
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1
agcttgccgc catgctgtat acctctcagc tgtaggact acttctgttt tggatctcg 60
cttcga 66

<210> 2
<211> 67
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 2
gatctcgaag cccgagatcc aaaacagaag tagtcctaac agctgagagg tatacagcat 60
ggcggca 67

<210> 3
<211> 34
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 3
gttgtcggat ccagaaaaca gctttgaaat gcaa

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<210> 4
<211> 44
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

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gttgtcggat ccaagaagg tggacaagat agaag                  35

<210> 6
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 6
ggatattgat gagatctagt gctacag                         27

<210> 7
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 7
gaacacagct cctattggat ccggtctttt ttctctttgc ac          42

<210> 8
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer
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cctgcatgga tccgatccgc cacotccaga acctccaccc cctgaaccgc ctccccctct 60
tttttctctt tgcactgttc ttctctttgc 90

<210> 9
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 9
gttattccat ggatccggac taatcttaca atgtgcttg 39

<210> 10
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 10
gtacagctaa atagatctgt agtaattaat tg 32

<210> 11
<211> 93
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

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aatgttacaa tgtgcttgg tgcattatac tcc 93

<210> 12
<211> 2252
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
HIV-human fusion construct

<220>
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<222> (13)..(2238)

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<220>
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<222> (13)..(72)

<220>
<221> mat_peptide
<222> (73)..(2238)

<220>
<221> misc_feature
<222> (73)..(1587)
<223> HIV gp120 allele + (Gly4Ser)3 linker

<220>
<221> misc_feature
<222> (1594)..(2238)
<223> CD154 extracellular domain from amino acids 48-261+Glu
      binds to CD40

<400> 12
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      Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe
      -20           -15           -10

tgg atc tcg gct tcg aga tct atg ctc ctt ggg ata ttg atg atc tgt  99
Trp Ile Ser Ala Ser Arg Ser Met Leu Leu Gly Ile Leu Met Ile Cys
      -5           -1           1           5

agt gct aca gaa aaa ttg tgg gtc aca gtc tat tat ggg gta cct gtg 147
Ser Ala Thr Glu Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val
      10          15          20          25

tgg aga gaa gca acc acc act cta ttt tgt gca tca gat gct aaa gcc 195
Trp Arg Glu Ala Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala
      30          35          40

tat gat aca gag gta cat aat gtt tgg gcc aca cat gcc tgt gta ccc 243
Tyr Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro
      45          50          55

aca gac ccc aac cca caa gaa gta gta ttg gga aat gtg aca gaa aat 291
Thr Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Asn
      60          65          70

ttt aac atg tgg aaa aat aac atg gta gat cag atg cat gag gat ata 339
Phe Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile
      75          80          85

atc agt tta tgg gat gaa agc cta aag cca tgt gta aaa tta acc cca 387
Ile Ser Leu Trp Asp Glu Ser Leu Lys Pro Cys Val Lys Leu Thr Pro
      90          95         100         105

ctc tgt gtt act tta aat tgc act aat ttg aat atc act aag aat act 435
Leu Cys Val Thr Leu Asn Cys Thr Asn Leu Asn Ile Thr Lys Asn Thr
      110         115         120

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act aat ccc act agt agc agc tgg gga atg atg gag aaa gga gaa ata		483	
Thr Asn Pro Thr Ser Ser Ser Trp Gly Met Met Glu Lys Gly Glu Ile			
125	130	135	
aaa aat tgc tct ttc tat atc acc aca agc ata aga aat aag gta aag		531	
Lys Asn Cys Ser Phe Tyr Ile Thr Thr Ser Ile Arg Asn Lys Val Lys			
140	145	150	
aaa gaa tat gca ctt ttt aat aga ctt gat gta gta cca ata gaa aat		579	
Lys Glu Tyr Ala Leu Phe Asn Arg Leu Asp Val Val Pro Ile Glu Asn			
155	160	165	
act aat aat act aag tat agg tta ata agt tgt aac acc tca gtc att		627	
Thr Asn Asn Thr Lys Tyr Arg Leu Ile Ser Cys Asn Thr Ser Val Ile			
170	175	180	185
aca cag gcc tgt cca aag gta tcc ttt cag cca att ccc ata cat tat		675	
Thr Gln Ala Cys Pro Lys Val Ser Phe Gln Pro Ile Pro Ile His Tyr			
190	195	200	
tgt gtc ccg gct ggg ttt gcg atg cta aag tgt aac aat aag aca ttc		723	
Cys Val Pro Ala Gly Phe Ala Met Leu Lys Cys Asn Asn Lys Thr Phe			
205	210	215	
aat gga tca gga cca tgc aca aat gtc agc aca gta caa tgt aca cat		771	
Asn Gly Ser Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His			
220	225	230	
gga att agg cca gtg gtg tca act caa ctg ctg tta aat ggc agt cta		819	
Gly Ile Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu			
235	240	245	
gca gaa gaa gac ata gta att aga tct gaa aat ttc aca gac aat gct		867	
Ala Glu Glu Asp Ile Val Ile Arg Ser Glu Asn Phe Thr Asp Asn Ala			
250	255	260	265
aaa acc ata ata gta cag cta aat gaa tct gta gta att aat tgt aca		915	
Lys Thr Ile Ile Val Gln Leu Asn Glu Ser Val Val Ile Asn Cys Thr			
270	275	280	
aga ccc aac aac aat aca aga aga agg tta tct ata gga cca ggg aga		963	
Arg Pro Asn Asn Asn Thr Arg Arg Leu Ser Ile Gly Pro Gly Arg			
285	290	295	
gca ttt tat gca aga aga aac ata ata gga gat ata aga caa gca cat		1011	
Ala Phe Tyr Ala Arg Arg Asn Ile Ile Gly Asp Ile Arg Gln Ala His			
300	305	310	
tgt aac att agt aga gca aaa tgg aat aac act tta caa cag ata gtt		1059	
Cys Asn Ile Ser Arg Ala Lys Trp Asn Asn Thr Leu Gln Gln Ile Val			
315	320	325	
ata aaa tta aga gaa aaa ttt agg aat aaa aca ata gcc ttt aat caa		1107	
Ile Lys Leu Arg Glu Lys Phe Arg Asn Lys Thr Ile Ala Phe Asn Gln			
330	335	340	345

tcc tca gga ggg gac cca gaa att gta atg cac agt ttt aat tgt gga		1155
Ser Ser Gly Gly Asp Pro Glu Ile Val Met His Ser Phe Asn Cys Gly		
350	355	360
ggg gaa ttc ttc tac tgt aat aca gca caa ctg ttt aat agt act tgg		1203
Gly Glu Phe Phe Tyr Cys Asn Thr Ala Gln Leu Phe Asn Ser Thr Trp		
365	370	375
aat gtt act gga ggg aca aat ggc act gaa gga aat gac ata atc aca		1251
Asn Val Thr Gly Gly Thr Asn Gly Thr Glu Gly Asn Asp Ile Ile Thr		
380	385	390
ctc caa tgc aga ata aaa caa att ata aat atg tgg cag aaa gta gga		1299
Leu Gln Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Lys Val Gly		
395	400	405
aaa gca atg tat gcc cct ccc atc aca gga caa att aga tgt tca tca		1347
Lys Ala Met Tyr Ala Pro Pro Ile Thr Gly Gln Ile Arg Cys Ser Ser		
410	415	420
425		
aat att aca ggg ctg cta cta aca aga gat gga ggt aat agt act gag		1395
Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Thr Glu		
430	435	440
act gag act gag atc ttc aga cct gga gga gga gat atg agg gac aat		1443
Thr Glu Thr Glu Ile Phe Arg Pro Gly Gly Asp Met Arg Asp Asn		
445	450	455
tgg aga agt gaa tta tat aaa tat aaa gta gta aga att gaa cca ata		1491
Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Arg Ile Glu Pro Ile		
460	465	470
gga gta gca ccc acc agg gca aag aga aga aca gtg caa aga gaa aaa		1539
Gly Val Ala Pro Thr Arg Ala Lys Arg Arg Thr Val Gln Arg Glu Lys		
475	480	485
aga ggg gga ggc ggt tca gga ggt ggt tct gga ggt ggc gga tcg		1587
Arg Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser		
490	495	500
505		
gat cca aga agg ttg gac aag ata gaa gat gaa agg aat ctt cat gaa		1635
Asp Pro Arg Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu		
510	515	520
gat ttt gta ttc atg aaa acg ata cag aga tgc aac aca gga gaa aga		1683
Asp Phe Val Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg		
525	530	535
tcc tta tcc tta ctg aac tgt gag gag att aaa agc cag ttt gaa ggc		1731
Ser Leu Ser Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly		
540	545	550
ttt gtg aag gat ata atg tta aac aaa gag gag acg aag aaa gaa aac		1779
Phe Val Lys Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn		
555	560	565

agc ttt gaa atg caa aaa ggt gat cag aat cct caa att gcg gca cat		1827
Ser Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His		
570	575	580
		585
gtc ata agt gag gcc agc agt aaa aca aca tct gtg tta cag tgg gct		1875
Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala		
590	595	600
gaa aaa gga tac tac acc atg agc aac aac ttg gta acc ctg gaa aat		1923
Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn		
605	610	615
ggg aaa cag ctg acc gtt aaa aga caa gga ctc tat tat atc tat gcc		1971
Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala		
620	625	630
caa gtc acc ttc tgt tcc aat cgg gaa gct tcg agt caa gct cca ttt		2019
Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe		
635	640	645
ata gcc agc ctc tgc cta aag tcc ccc ggt aga ttc gag aga atc tta		2067
Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu		
650	655	660
		665
ctc aga gct gca aat acc cac agt tcc gcc aaa cct tgc ggg caa caa		2115
Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln		
670	675	680
tcc att cac ttg gga gga gta ttt gaa ttg caa cca ggt gct tcg gtg		2163
Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val		
685	690	695
ttt gtc aat gtg act gat cca agc caa gtg agc cat ggc act ggc ttc		2211
Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe		
700	705	710
acg tcc ttt ggc tta ctc aaa ctc gag tgataatcta gata		2252
Thr Ser Phe Gly Leu Leu Lys Leu Glu		
715	720	

<210> 13
 <211> 2208
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 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 HIV-human fusion construct

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 <221> CDS
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<222> (73)..(1545)
<223> HIV gp120 allele + ProAspPro linker

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<222> (1552)..(2196)
<223> CD154 extracellular domain long form (amino acids 48-261)+Glu
      binds to CD40

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      Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe
      -20           -15           -10

tgg atc tcg gct tcg aga tcc atg ctc ctt ggg ata ttg atg atc tgt  99
Trp Ile Ser Ala Ser Arg Ser Met Leu Leu Gly Ile Leu Met Ile Cys
      -5           -1           1           5

agt gct aca gaa aaa ttg tgg gtc aca gtc tat tat ggg gta cct gtg 147
Ser Ala Thr Glu Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val
      10          15          20          25

tgg aga gaa gca acc acc act cta ttt tgt gca tca gat gct aaa gcc 195
Trp Arg Glu Ala Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala
      30          35          40

tat gat aca gag gta cat aat gtt tgg gcc aca cat gcc tgt gta ccc 243
Tyr Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro
      45          50          55

aca gac ccc aac cca caa gaa gta gta ttg gga aat gtg aca gaa aat 291
Thr Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Asn
      60          65          70

ttt aac atg tgg aaa aat aac atg gta gat cag atg cat gag gat ata 339
Phe Asn Met Trp Lys Asn Asn Val Asp Gln Met His Glu Asp Ile
      75          80          85

atc agt tta tgg gat gaa agc cta aag cca tgt gta aaa tta acc cca 387
Ile Ser Leu Trp Asp Glu Ser Leu Lys Pro Cys Val Lys Leu Thr Pro
      90          95         100         105

ctc tgt gtt act tta aat tgc act aat ttg aat atc act aag aat act 435
Leu Cys Val Thr Leu Asn Cys Thr Asn Leu Asn Ile Thr Lys Asn Thr
      110         115         120

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act aat ccc act agt agc agc tgg gga atg atg gag aaa gga gaa ata		483
Thr Asn Pro Thr Ser Ser Ser Trp Gly Met Met Glu Lys Gly Glu Ile		
125	130	135
aaa aat tgc tct ttc tat atc acc aca agc ata aga aat aag gta aag		531
Lys Asn Cys Ser Phe Tyr Ile Thr Thr Ser Ile Arg Asn Lys Val Lys		
140	145	150
aaa gaa tat gca ctt ttt aat aga ctt gat gta gta cca ata gaa aat		579
Lys Glu Tyr Ala Leu Phe Asn Arg Leu Asp Val Val Pro Ile Glu Asn		
155	160	165
act aat aat act aag tat agg tta ata agt tgt aac acc tca gtc att		627
Thr Asn Asn Thr Lys Tyr Arg Leu Ile Ser Cys Asn Thr Ser Val Ile		
170	175	180
185		
aca cag gcc tgt cca aag gta tcc ttt cag cca att ccc ata cat tat		675
Thr Gln Ala Cys Pro Lys Val Ser Phe Gln Pro Ile Pro Ile His Tyr		
190	195	200
tgt gtc ccg gct ggg ttt gcg atg cta aag tgt aac aat aag aca ttc		723
Cys Val Pro Ala Gly Phe Ala Met Leu Lys Cys Asn Asn Lys Thr Phe		
205	210	215
aat gga tca gga cca tgc aca aat gtc agc aca gta caa tgt aca cat		771
Asn Gly Ser Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His		
220	225	230
gga att agg cca gtg gtg tca act caa ctg ctg tta aat ggc agt cta		819
Gly Ile Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu		
235	240	245
gca gaa gaa gac ata gta att aga tct gaa aat ttc aca gac aat gct		867
Ala Glu Glu Asp Ile Val Ile Arg Ser Glu Asn Phe Thr Asp Asn Ala		
250	255	260
265		
aaa acc ata ata gta cag cta aat gaa tct gta gta att aat tgt aca		915
Lys Thr Ile Ile Val Gln Leu Asn Glu Ser Val Val Ile Asn Cys Thr		
270	275	280
aga ccc aac aac aat aca aga aga agg tta tct ata gga cca ggg aga		963
Arg Pro Asn Asn Asn Thr Arg Arg Leu Ser Ile Gly Pro Gly Arg		
285	290	295
gca ttt tat gca aga aga aac ata ata gga gat ata aga caa gca cat		1011
Ala Phe Tyr Ala Arg Arg Asn Ile Ile Gly Asp Ile Arg Gln Ala His		
300	305	310
tgt aac att agt aga gca aaa tgg aat aac act tta caa cag ata gtt		1059
Cys Asn Ile Ser Arg Ala Lys Trp Asn Asn Thr Leu Gln Gln Ile Val		
315	320	325
ata aaa tta aga gaa aaa ttt agg aat aaa aca ata gcc ttt aat caa		1107
Ile Lys Leu Arg Glu Lys Phe Arg Asn Lys Thr Ile Ala Phe Asn Gln		
330	335	340
345		

tcc tca gga ggg gac cca gaa att gta atg cac agt ttt aat tgt gga		1155	
Ser Ser Gly Gly Asp Pro Glu Ile Val Met His Ser Phe Asn Cys Gly			
350	355	360	
ggg gaa ttc ttc tac tgt aat aca gca caa ctg ttt aat agt act tgg		1203	
Gly Glu Phe Phe Tyr Cys Asn Thr Ala Gln Leu Phe Asn Ser Thr Trp			
365	370	375	
aat gtt act gga ggg aca aat ggc act gaa gga aat gac ata atc aca		1251	
Asn Val Thr Gly Gly Thr Asn Gly Thr Glu Gly Asn Asp Ile Ile Thr			
380	385	390	
ctc caa tgc aga ata aaa caa att ata aat atg tgg cag aaa gta gga		1299	
Leu Gln Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Lys Val Gly			
395	400	405	
aaa gca atg tat gcc cct ccc atc aca gga caa att aga tgt tca tca		1347	
Lys Ala Met Tyr Ala Pro Pro Ile Thr Gly Gln Ile Arg Cys Ser Ser			
410	415	420	425
aat att aca ggg ctg cta cta aca aga gat gga ggt aat agt act gag		1395	
Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Thr Glu			
430	435	440	
act gag act gag atc ttc aga cct gga gga gat atg agg gac aat		1443	
Thr Glu Thr Glu Ile Phe Arg Pro Gly Gly Asp Met Arg Asp Asn			
445	450	455	
tgg aga agt gaa tta tat aaa tat aaa gta gta aga att gaa cca ata		1491	
Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Arg Ile Glu Pro Ile			
460	465	470	
gga gta gca ccc acc agg gca aag aga aga aca gtg caa aga gaa aaa		1539	
Gly Val Ala Pro Thr Arg Ala Lys Arg Arg Thr Val Gln Arg Glu Lys			
475	480	485	
aga ccg gat cca aga agg ttg gac aag ata gaa gat gaa agg aat ctt		1587	
Arg Pro Asp Pro Arg Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu			
490	495	500	505
cat gaa gat ttt gta ttc atg aaa acg ata cag aga tgc aac aca gga		1635	
His Glu Asp Phe Val Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly			
510	515	520	
gaa aga tcc tta tcc tta ctg aac tgt gag gag att aaa agc cag ttt		1683	
Glu Arg Ser Leu Ser Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe			
525	530	535	
gaa ggc ttt gtg aag gat ata atg tta aac aaa gag gag acg aag aaa		1731	
Glu Gly Phe Val Lys Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys			
540	545	550	
gaa aac agc ttt gaa atg caa aaa ggt gat cag aat cct caa att gcg		1779	
Glu Asn Ser Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala			
555	560	565	

gca cat gtc ata agt gag gcc agc agt aaa aca aca tct gtg tta cag		1827	
Ala His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln			
570	575	580	585
tgg gct gaa aaa gga tac tac acc atg agc aac aac ttg gta acc ctg		1875	
Trp Ala Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu			
590	595	600	
gaa aat ggg aaa cag ctg acc gtt aaa aga caa gga ctc tat tat atc		1923	
Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile			
605	610	615	
tat gcc caa gtc acc ttc tgt tcc aat cggt gaa gct tcg agt caa gct		1971	
Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala			
620	625	630	
cca ttt ata gcc agc ctc tgc cta aag tcc ccc ggt aga ttc gag aga		2019	
Pro Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg			
635	640	645	
atc tta ctc aga gct gca aat acc cac agt tcc gcc aaa cct tgc ggg		2067	
Ile Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly			
650	655	660	665
caa caa tcc att cac ttg gga gga gta ttt gaa ttg caa cca ggt gct		2115	
Gln Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala			
670	675	680	
tcg gtg ttt gtc aat gtg act gat cca agc caa gtg agc cat ggc act		2163	
Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr			
685	690	695	
ggc ttc acg tcc ttt ggc tta ctc aaa ctc gag tgataatcta ga		2208	
Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu Glu			
700	705		

<210> 14
<211> 2070
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
HIV-human fusion construct

<220>
<221> CDS
<222> (13)..(2058)

<220>
<221> sig_peptide
<222> (13)..(72)

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<220>
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<220>
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<222> (73)..(1587)
<223> HIV gp120 allele + (Gly4Ser)3 linker

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<222> (1594)..(2058)
<223> CD154 extracellular domain from amino acids 108-261+Glu
      binds to CD40

<400> 14
aagcttgcgg cc atg ctg tat acc tct cag ctg tta gga cta ctt ctg ttt 51
      Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe
      -20           -15           -10

tgg atc tcg gct tcg aga tct atg ctc ctt ggg ata ttg atg atc tgt 99
Trp Ile Ser Ala Ser Arg Ser Met Leu Leu Gly Ile Leu Met Ile Cys
      -5           -1           1           5

agt gct aca gaa aaa ttg tgg gtc aca gtc tat tat ggg gta cct gtg 147
Ser Ala Thr Glu Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val
      10          15          20          25

tgg aga gaa gca acc acc act cta ttt tgt gca tca gat gct aaa gcc 195
Trp Arg Glu Ala Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala
      30          35          40

tat gat aca gag gta cat aat gtt tgg gcc aca cat gcc tgt gta ccc 243
Tyr Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro
      45          50          55

aca gac ccc aac cca caa gaa gta gta ttg gga aat gtg aca gaa aat 291
Thr Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Asn
      60          65          70

ttt aac atg tgg aaa aat aac atg gta gat cag atg cat gag gat ata 339
Phe Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile
      75          80          85

atc agt tta tgg gat gaa agc cta aag cca tgt gta aaa tta acc cca 387
Ile Ser Leu Trp Asp Glu Ser Leu Lys Pro Cys Val Lys Leu Thr Pro
      90          95         100         105

ctc tgt gtt act tta aat tgc act aat ttg aat atc act aag aat act 435
Leu Cys Val Thr Leu Asn Cys Thr Asn Leu Asn Ile Thr Lys Asn Thr
      110         115         120

act aat ccc act agt agc agc tgg gga atg atg gag aaa gga gaa ata 483
Thr Asn Pro Thr Ser Ser Ser Trp Gly Met Met Glu Lys Gly Glu Ile
      125         130         135

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aaa aat tgc tct ttc tat atc acc aca agc ata aga aat aag gta aag		531	
Lys Asn Cys Ser Phe Tyr Ile Thr Thr Ser Ile Arg Asn Lys Val Lys			
140	145	150	
aaa gaa tat gca ctt ttt aat aga ctt gat gta gta cca ata gaa aat		579	
Lys Glu Tyr Ala Leu Phe Asn Arg Leu Asp Val Val Pro Ile Glu Asn			
155	160	165	
act aat aat act aag tat agg tta ata agt tgt aac acc tca gtc att		627	
Thr Asn Asn Thr Lys Tyr Arg Leu Ile Ser Cys Asn Thr Ser Val Ile			
170	175	180	185
aca cag gcc tgt cca aag gta tcc ttt cag cca att ccc ata cat tat		675	
Thr Gln Ala Cys Pro Lys Val Ser Phe Gln Pro Ile Pro Ile His Tyr			
190	195	200	
tgt gtc ccg gct ggg ttt gcg atg cta aag tgt aac aat aag aca ttc		723	
Cys Val Pro Ala Gly Phe Ala Met Leu Lys Cys Asn Asn Lys Thr Phe			
205	210	215	
aat gga tca gga cca tgc aca aat gtc agc aca gta caa tgt aca cat		771	
Asn Gly Ser Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His			
220	225	230	
gga att agg cca gtg gtg tca act caa ctg ctg tta aat ggc agt cta		819	
Gly Ile Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu			
235	240	245	
gca gaa gaa gac ata gta att aga tct gaa aat ttc aca gac aat gct		867	
Ala Glu Glu Asp Ile Val Ile Arg Ser Glu Asn Phe Thr Asp Asn Ala			
250	255	260	265
aaa acc ata ata gta cag cta aat gaa tct gta gta att aat tgt aca		915	
Lys Thr Ile Ile Val Gln Leu Asn Glu Ser Val Val Ile Asn Cys Thr			
270	275	280	
aga ccc aac aac aat aca aga aga agg tta tct ata gga cca ggg aga		963	
Arg Pro Asn Asn Asn Thr Arg Arg Leu Ser Ile Gly Pro Gly Arg			
285	290	295	
gca ttt tat gca aga aga aac ata ata gga gat ata aga caa gca cat		1011	
Ala Phe Tyr Ala Arg Arg Asn Ile Ile Gly Asp Ile Arg Gln Ala His			
300	305	310	
tgt aac att agt aga gca aaa tgg aat aac act tta caa cag ata gtt		1059	
Cys Asn Ile Ser Arg Ala Lys Trp Asn Asn Thr Leu Gln Gln Ile Val			
315	320	325	
ata aaa tta aga gaa aaa ttt agg aat aaa aca ata gcc ttt aat caa		1107	
Ile Lys Leu Arg Glu Lys Phe Arg Asn Lys Thr Ile Ala Phe Asn Gln			
330	335	340	345
tcc tca gga ggg gac cca gaa att gta atg cac agt ttt aat tgt gga		1155	
Ser Ser Gly Gly Asp Pro Glu Ile Val Met His Ser Phe Asn Cys Gly			
350	355	360	

ggg gaa ttc ttc tac tgt aat aca gca caa ctg ttt aat agt act tgg		1203	
Gly Glu Phe Phe Tyr Cys Asn Thr Ala Gln Leu Phe Asn Ser Thr Trp			
365	370	375	
aat gtt act gga ggg aca aat ggc act gaa gga aat gac ata atc aca		1251	
Asn Val Thr Gly Gly Thr Asn Gly Thr Glu Gly Asn Asp Ile Ile Thr			
380	385	390	
ctc caa tgc aga ata aaa caa att ata aat atg tgg cag aaa gta gga		1299	
Leu Gln Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Lys Val Gly			
395	400	405	
aaa gca atg tat gcc cct ccc atc aca gga caa att aga tgt tca tca		1347	
Lys Ala Met Tyr Ala Pro Pro Ile Thr Gly Gln Ile Arg Cys Ser Ser			
410	415	420	425
aat att aca ggg ctg cta cta aca aga gat gga ggt aat agt act gag		1395	
Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Thr Glu			
430	435	440	
act gag act gag atc ttc aga cct gga gga gga gat atg agg gac aat		1443	
Thr Glu Thr Glu Ile Phe Arg Pro Gly Gly Asp Met Arg Asp Asn			
445	450	455	
tgg aga agt gaa tta tat aaa tat aaa gta gta aga att gaa cca ata		1491	
Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Arg Ile Glu Pro Ile			
460	465	470	
gga gta gca ccc acc agg gca aag aga aga aca gtg caa aga gaa aaa		1539	
Gly Val Ala Pro Thr Arg Ala Lys Arg Arg Thr Val Gln Arg Glu Lys			
475	480	485	
aga ggg gga ggc ggt tca gga ggt gga ggt tct gga ggt ggc gga tcg		1587	
Arg Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Ser			
490	495	500	505
gat cca gaa aac agc ttt gaa atg caa aaa ggt gat cag aat cct caa		1635	
Asp Pro Glu Asn Ser Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln			
510	515	520	
att gcg gca cat gtc ata agt gag gcc agc agt aaa aca aca tct gtg		1683	
Ile Ala Ala His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val			
525	530	535	
tta cag tgg gct gaa aaa gga tac tac acc atg agc aac aac ttg gta		1731	
Leu Gln Trp Ala Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val			
540	545	550	
acc ctg gaa aat ggg aaa cag ctg acc gtt aaa aga caa gga ctc tat		1779	
Thr Leu Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr			
555	560	565	
tat atc tat gcc caa gtc acc ttc tgt tcc aat cgg gaa gct tcg agt		1827	
Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser			
570	575	580	585

caa gct cca ttt ata gcc agc ctc tgc cta aag tcc ccc ggt aga ttc	1875
Gln Ala Pro Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe	
590	595
	600
gag aga atc tta ctc aga gct gca aat acc cac agt tcc gcc aaa cct	1923
Glu Arg Ile Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro	
605	610
	615
tgc ggg caa caa tcc att cac ttg gga gga gta ttt gaa ttg caa cca	1971
Cys Gly Gln Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro	
620	625
	630
ggt gct tcg gtg ttt gtc aat gtg act gat cca agc caa gtg agc cat	2019
Gly Ala Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His	
635	640
	645
ggc act ggc ttc acg tcc ttt ggc tta ctc aaa ctc gag tgataatcta ga	2070
Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu Glu	
650	655
	660

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<210> 15
<211> 2028
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      HIV-human fusion construct

<220>
<221> CDS
<222> (13)..(2016)

<220>
<221> sig_peptide
<222> (13)..(72)

<220>
<221> mat_peptide
<222> (73)..(2016)

<220>
<221> misc_feature
<222> (73)..(1551)
<223> HIV gp120 allele + ProAspPro linker

<220>
<221> misc_feature
<222> (1552)..(2016)
<223> CD154 extracellular domain from amino acids 108-261+Glu
      binds to CD40

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<400> 15
 aagcttgcgg cc atg ctg tat acc tct cag ctg tta gga cta ctt ctg ttt 51
 Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe
 -20 -15 -10

tgg atc tcg gct tcg aga tcc atg ctc ctt ggg ata ttg atg atc tgt 99
 Trp Ile Ser Ala Ser Arg Ser Met Leu Leu Gly Ile Leu Met Ile Cys
 -5 -1 1 5

agt gct aca gaa aaa ttg tgg gtc aca gtc tat tat ggg gta cct gtg 147
 Ser Ala Thr Glu Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val
 10 15 20 25

tgg aga gaa gca acc acc act cta ttt tgt gca tca gat gct aaa gcc 195
 Trp Arg Glu Ala Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala
 30 35 40

tat gat aca gag gta cat aat gtt tgg gcc aca cat gcc tgt gta ccc 243
 Tyr Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro
 45 50 55

aca gac ccc aac cca caa gaa gta gta ttg gga aat gtg aca gaa aat 291
 Thr Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Asn
 60 65 70

ttt aac atg tgg aaa aat aac atg gta gat cag atg cat gag gat ata 339
 Phe Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile
 75 80 85

atc agt tta tgg gat gaa agc cta aag cca tgt gta aaa tta acc cca 387
 Ile Ser Leu Trp Asp Glu Ser Leu Lys Pro Cys Val Lys Leu Thr Pro
 90 95 100 105

ctc tgt gtt act tta aat tgc act aat ttg aat atc act aag aat act 435
 Leu Cys Val Thr Leu Asn Cys Thr Asn Leu Asn Ile Thr Lys Asn Thr
 110 115 120

act aat ccc act agt agc agc tgg gga atg atg gag aaa gga gaa ata 483
 Thr Asn Pro Thr Ser Ser Trp Gly Met Met Glu Lys Gly Glu Ile
 125 130 135

aaa aat tgc tct ttc tat atc acc aca agc ata aga aat aag gta aag 531
 Lys Asn Cys Ser Phe Tyr Ile Thr Ser Ile Arg Asn Lys Val Lys
 140 145 150

aaa gaa tat gca ctt ttt aat aga ctt gat gta gta cca ata gaa aat 579
 Lys Glu Tyr Ala Leu Phe Asn Arg Leu Asp Val Val Pro Ile Glu Asn
 155 160 165

act aat aat act aag tat agg tta ata agt tgt aac acc tca gtc att 627
 Thr Asn Asn Thr Lys Tyr Arg Leu Ile Ser Cys Asn Thr Ser Val Ile
 170 175 180 185

aca cag gcc tgt cca aag gta tcc ttt cag cca att ccc ata cat tat 675
 Thr Gln Ala Cys Pro Lys Val Ser Phe Gln Pro Ile Pro Ile His Tyr
 190 195 200

tgt gtc ccg gct ggg ttt gcg atg cta aag tgt aac aat aag aca ttc		723	
Cys Val Pro Ala Gly Phe Ala Met Leu Lys Cys Asn Asn Lys Thr Phe			
205	210	215	
aat gga tca gga cca tgc aca aat gtc agc aca gta caa tgt aca cat		771	
Asn Gly Ser Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His			
220	225	230	
gga att agg cca gtg gtg tca act caa ctg ctg tta aat ggc agt cta		819	
Gly Ile Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu			
235	240	245	
gca gaa gaa gac ata gta att aga tct gaa aat ttc aca gac aat gct		867	
Ala Glu Glu Asp Ile Val Ile Arg Ser Glu Asn Phe Thr Asp Asn Ala			
250	255	260	265
aaa acc ata ata gta cag cta aat gaa tct gta gta att aat tgt aca		915	
Lys Thr Ile Ile Val Gln Leu Asn Glu Ser Val Val Ile Asn Cys Thr			
270	275	280	
aga ccc aac aac aat aca aga aga agg tta tct ata gga cca ggg aga		963	
Arg Pro Asn Asn Asn Thr Arg Arg Arg Leu Ser Ile Gly Pro Gly Arg			
285	290	295	
gca ttt tat gca aga aga aac ata ata gga gat ata aga caa gca cat		1011	
Ala Phe Tyr Ala Arg Arg Asn Ile Ile Gly Asp Ile Arg Gln Ala His			
300	305	310	
tgt aac att agt aga gca aaa tgg aat aac act tta caa cag ata gtt		1059	
Cys Asn Ile Ser Arg Ala Lys Trp Asn Asn Thr Leu Gln Gln Ile Val			
315	320	325	
ata aaa tta aga gaa aaa ttt agg aat aaa aca ata gcc ttt aat caa		1107	
Ile Lys Leu Arg Glu Lys Phe Arg Asn Lys Thr Ile Ala Phe Asn Gln			
330	335	340	345
tcc tca gga ggg gac cca gaa att gta atg cac agt ttt aat tgt gga		1155	
Ser Ser Gly Gly Asp Pro Glu Ile Val Met His Ser Phe Asn Cys Gly			
350	355	360	
ggg gaa ttc ttc tac tgt aat aca gca caa ctg ttt aat agt act tgg		1203	
Gly Glu Phe Phe Tyr Cys Asn Thr Ala Gln Leu Phe Asn Ser Thr Trp			
365	370	375	
aat gtt act gga ggg aca aat ggc act gaa gga aat gac ata atc aca		1251	
Asn Val Thr Gly Gly Thr Asn Gly Thr Glu Gly Asn Asp Ile Ile Thr			
380	385	390	
ctc caa tgc aga ata aaa caa att ata aat atg tgg cag aaa gta gga		1299	
Leu Gln Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Lys Val Gly			
395	400	405	
aaa gca atg tat gcc cct ccc atc aca gga caa att aga tgt tca tca		1347	
Lys Ala Met Tyr Ala Pro Pro Ile Thr Gly Gln Ile Arg Cys Ser Ser			
410	415	420	425

aat att aca ggg ctg cta cta aca aga gat gga ggt aat agt act gag Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Thr Glu 430 435 440	1395
act gag act gag atc ttc aga cct gga gga gat atg agg gac aat Thr Glu Thr Glu Ile Phe Arg Pro Gly Gly Asp Met Arg Asp Asn 445 450 455	1443
tgg aga agt gaa tta tat aaa tat aaa gta gta aga att gaa cca ata Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Arg Ile Glu Pro Ile 460 465 470	1491
gga gta gca ccc acc agg gca aag aga aca gtg caa aga gaa aaa Gly Val Ala Pro Thr Arg Ala Lys Arg Arg Thr Val Gln Arg Glu Lys 475 480 485	1539
aga ccg gat cca gaa aac agc ttt gaa atg caa aaa ggt gat cag aat Arg Pro Asp Pro Glu Asn Ser Phe Glu Met Gln Lys Gly Asp Gln Asn 490 495 500 505	1587
cct caa att gcg gca cat gtc ata agt gag gcc agc agt aaa aca aca Pro Gln Ile Ala Ala His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr 510 515 520	1635
tct gtg tta cag tgg gct gaa aaa gga tac tac acc atg agc aac aac Ser Val Leu Gln Trp Ala Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn 525 530 535	1683
ttg gta acc ctg gaa aat ggg aaa cag ctg acc gtt aaa aga caa gga Leu Val Thr Leu Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly 540 545 550	1731
ctc tat tat atc tat gcc caa gtc acc ttc tgt tcc aat cgg gaa gct Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala 555 560 565	1779
tcg agt caa gct cca ttt ata gcc agc ctc tgc cta aag tcc ccc ggt Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly 570 575 580 585	1827
aga ttc gag aga atc tta ctc aga gct gca aat acc cac agt tcc gcc Arg Phe Glu Arg Ile Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala 590 595 600	1875
aaa cct tgc ggg caa caa tcc att cac ttg gga gga gta ttt gaa ttg Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu 605 610 615	1923
caa cca ggt gct tcg gtg ttt gtc aat gtg act gat cca agc caa gtg Gln Pro Gly Ala Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val 620 625 630	1971
agc cat ggc act ggc ttc acg tcc ttt ggc tta ctc aaa ctc gag Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu Glu 635 640 645	2016
tgataatcta ga	2028

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<210> 16
<211> 906
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      HIV-human fusion construct

<220>
<221> CDS
<222> (13)..(894)

<220>
<221> sig_peptide
<222> (13)..(72)

<220>
<221> mat_peptide
<222> (73)..(894)

<220>
<221> misc_feature
<222> (73)..(243)
<223> HIV gp120 V3 loop + (Gly4Ser)3 linker

<220>
<221> misc_feature
<222> (250)..(894)
<223> CD154 extracellular domain from amino acids 48-261+Glu
      binds to CD40

<400> 16
aagcttgcgg cc atg ctg tat acc tct cag ctg tta gga cta ctt ctg ttt 51
      Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe
      -20           -15           -10

tgg atc tcg gct tcg aga tct gta gta att aat tgt aca aga ccc aac  99
Trp Ile Ser Ala Ser Arg Ser Val Val Ile Asn Cys Thr Arg Pro Asn
      -5           -1           1           5

aac aat aca aga aga agg tta tct ata gga cca ggg aga gca ttt tat 147
Asn Asn Thr Arg Arg Leu Ser Ile Gly Pro Gly Arg Ala Phe Tyr
      10          15          20          25

gca aga aga aac ata ata gga gat ata aga caa gca cat tgt aac att 195
Ala Arg Arg Asn Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile
      30          35          40

agt ggt ggc ggt ggc tca gga ggc ggt gga tct ggc ggt gga ggt tcg 243
Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser
      45          50          55

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gat cca aga agg ttg gac aag ata gaa gat gaa agg aat ctt cat gaa	291
Asp Pro Arg Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu	
60 65 70	
gat ttt gta ttc atg aaa acg ata cag aga tgc aac aca gga gaa aga	339
Asp Phe Val Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg	
75 80 85	
tcc tta tcc tta ctg aac tgt gag gag att aaa agc cag ttt gaa ggc	387
Ser Leu Ser Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly	
90 95 100 105	
ttt gtg aag gat ata atg tta aac aaa gag gag acg aag aaa gaa aac	435
Phe Val Lys Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn	
110 115 120	
agc ttt gaa atg caa aaa ggt gat cag aat cct caa att gcg gca cat	483
Ser Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His	
125 130 135	
gtc ata agt gag gcc agc agt aaa aca aca tct gtg tta cag tgg gct	531
Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala	
140 145 150	
gaa aaa gga tac tac acc atg agc aac aac ttg gta acc ctg gaa aat	579
Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn	
155 160 165	
ggg aaa cag ctg acc gtt aaa aga caa gga ctc tat tat atc tat gcc	627
Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala	
170 175 180 185	
caa gtc acc ttc tgt tcc aat cgg gaa gct tcg agt caa gct cca ttt	675
Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe	
190 195 200	
ata gcc agc ctc tgc cta aag tcc ccc ggt aga ttc gag aga atc tta	723
Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu	
205 210 215	
ctc aga gct gca aat acc cac agt tcc gcc aaa cct tgc ggg caa caa	771
Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln	
220 225 230	
tcc att cac ttg gga gga gta ttt gaa ttg caa cca ggt gct tcg gtg	819
Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val	
235 240 245	
ttt gtc aat gtg act gat cca agc caa gtg agc cat ggc act ggc ttc	867
Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe	
250 255 260 265	
acg tcc ttt ggc tta ctc aaa ctc gag tgataatcta ga	906
Thr Ser Phe Gly Leu Leu Lys Leu Glu	
270	

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<210> 17
<211> 864
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      HIV-human fusion construct

<220>
<221> CDS
<222> (13)..(852)

<220>
<221> sig_peptide
<222> (13)..(72)

<220>
<221> mat_peptide
<222> (73)..(852)

<220>
<221> misc_feature
<222> (73)..(207)
<223> HIV gp120 allele + (Gly4Ser)3 linker

<220>
<221> misc_feature
<222> (208)..(852)
<223> CD154 extracellular domain from amino acids 48-261+Glu
      binds to CD40

<400> 17
aagcttgcgg cc atg ctg tat acc tct cag ctg tta gga cta ctt ctg ttt 51
      Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Phe
      -20           -15           -10

tgg atc tcg gct tcg aga tct gta gta att aat tgt aca aga ccc aac  99
Trp Ile Ser Ala Ser Arg Ser Val Val Ile Asn Cys Thr Arg Pro Asn
      -5           -1           1           5

aac aat aca aga aga agg tta tct ata gga cca ggg aga gca ttt tat 147
Asn Asn Thr Arg Arg Leu Ser Ile Gly Pro Gly Arg Ala Phe Tyr
      10          15          20          25

gca aga aga aac ata ata gga gat ata aga caa gca cat tgt aac att 195
Ala Arg Arg Asn Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile
      30          35          40

agt ccg gat cca aga agg ttg gac aag ata gaa gat gaa agg aat ctt 243
Ser Pro Asp Pro Arg Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu
      45          50          55

cat gaa gat ttt gta ttc atg aaa acg ata cag aga tgc aac aca gga 291
His Glu Asp Phe Val Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly
      60          65          70

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gaa aga tcc tta tcc tta ctg aac tgt gag gag att aaa agc cag ttt		339	
Glu Arg Ser Leu Ser Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe			
75	80	85	
gaa ggc ttt gtg aag gat ata atg tta aac aaa gag gag acg aag aaa		387	
Glu Gly Phe Val Lys Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys			
90	95	100	105
gaa aac agc ttt gaa atg caa aaa ggt gat cag aat cct caa att gcg		435	
Glu Asn Ser Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala			
110	115	120	
gca cat gtc ata agt gag gcc agc agt aaa aca aca tct gtg tta cag		483	
Ala His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln			
125	130	135	
tgg gct gaa aaa gga tac tac acc atg agc aac aac ttg gta acc ctg		531	
Trp Ala Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu			
140	145	150	
gaa aat ggg aaa cag ctg acc gtt aaa aga caa gga ctc tat tat atc		579	
Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile			
155	160	165	
tat gcc caa gtc acc ttc tgt tcc aat cgg gaa gct tcg agt caa gct		627	
Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala			
170	175	180	185
cca ttt ata gcc agc ctc tgc cta aag tcc ccc ggt aga ttc gag aga		675	
Pro Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg			
190	195	200	
atc tta ctc aga gct gca aat acc cac agt tcc gcc aaa cct tgc ggg		723	
Ile Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly			
205	210	215	
caa caa tcc att cac ttg gga gga gta ttt gaa ttg caa cca ggt gct		771	
Gln Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala			
220	225	230	
tcg gtg ttt gtc aat gtg act gat cca agc caa gtg agc cat ggc act		819	
Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr			
235	240	245	
ggc ttc acg tcc ttt ggc tta ctc aaa ctc gag tgataatcta ga		864	
Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu Glu			
250	255	260	

<210> 18
 <211> 726
 <212> DNA
 <213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
      HIV-human fusion construct

<220>
<221> CDS
<222> (13)..(714)

<220>
<221> sig_peptide
<222> (13)..(72)

<220>
<221> mat_peptide
<222> (73)..(714)

<220>
<221> misc_feature
<222> (73)..(207)
<223> HIV gp120 V3 loop + ProAspPro linker

<220>
<221> misc_feature
<222> (208)..(714)
<223> CD154 extracellular domain from amino acids 108-261+Glu
      binds to CD40

<400> 18
aagcttgcgg cc atg ctg tat acc tct cag ctg tta gga cta ctt ctg ttt 51
      Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe
      -20           -15           -10

tgg atc tcg gct tcg aga tct gta gta att aat tgt aca aga ccc aac   99
Trp Ile Ser Ala Ser Arg Ser Val Val Ile Asn Cys Thr Arg Pro Asn
      -5           -1           1           5

aac aat aca aga aga agg tta tct ata gga cca ggg aga gca ttt tat  147
Asn Asn Thr Arg Arg Leu Ser Ile Gly Pro Gly Arg Ala Phe Tyr
      10          15          20          25

gca aga aga aac ata ata gga gat ata aga caa gca cat tgt aac att  195
Ala Arg Arg Asn Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile
      30          35          40

agt ggt ggc ggt ggc tca gga ggc ggt gga tct ggc ggt gga ggt tcg  243
Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser
      45          50          55

gat cca gaa aac agc ttt gaa atg caa aaa ggt gat cag aat cct caa  291
Asp Pro Glu Asn Ser Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln
      60          65          70

att gcg gca cat gtc ata agt gag gcc agc agt aaa aca aca tct gtg  339
Ile Ala Ala His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val
      75          80          85

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tta cag tgg gct gaa aaa gga tac tac acc acc atg agc aac aac ttg gta	387
Leu Gln Trp Ala Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val	
90 95 100 105	
acc ctg gaa aat ggg aaa cag ctg acc gtt aaa aga caa gga ctc tat	435
Thr Leu Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr	
110 115 120	
tat atc tat gcc caa gtc acc ttc tgt tcc aat cgg gaa gct tcg agt	483
Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser	
125 130 135	
caa gct cca ttt ata gcc agc ctc tgc cta aag tcc ccc ggt aga ttc	531
Gln Ala Pro Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe	
140 145 150	
gag aga atc tta ctc aga gct gca aat acc cac agt tcc gcc aaa cct	579
Glu Arg Ile Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro	
155 160 165	
tgc ggg caa caa tcc att cac ttg gga gga gta ttt gaa ttg caa cca	627
Cys Gly Gln Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro	
170 175 180 185	
ggt gct tcg gtg ttt gtc aat gtg act gat cca agc caa gtg agc cat	675
Gly Ala Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His	
190 195 200	
ggc act ggc ttc acg tcc ttt ggc tta ctc aaa ctc gag tgataatcta ga	726
Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu Glu	
205 210	

<210> 19
<211> 684
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
HIV-human fusion construct

<220>
<221> CDS
<222> (13)..(672)

<220>
<221> sig_peptide
<222> (13)..(72)

<220>
<221> mat_peptide
<222> (73)..(672)

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<220>
<221> misc_feature
<222> (73)..(207)
<223> HIV gp120 V3 loop + ProAspPro linker

<220>
<221> misc_feature
<222> (208)..(672)
<223> CD154 extracellular domain from amino acids 108-261+Glu
      binds to CD40

<400> 19
aagcttgcgg cc atg ctg tat acc tct cag ctg tta gga cta ctt ctg ttt 51
      Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Phe
      -20          -15           -10

tgg atc tcg gct tcg aga tct gta gta att aat tgt aca aga ccc aac  99
Trp Ile Ser Ala Ser Arg Ser Val Val Ile Asn Cys Thr Arg Pro Asn
      -5           -1       1           5

aac aat aca aga aga agg tta tct ata gga cca ggg aga gca ttt tat 147
Asn Asn Thr Arg Arg Leu Ser Ile Gly Pro Gly Arg Ala Phe Tyr
      10          15           20           25

gca aga aga aac ata ata gga gat ata aga caa gca cat tgt aac att 195
Ala Arg Arg Asn Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile
      30          35           40

agt ccg gat cca gaa aac agc ttt gaa atg caa aaa ggt gat cag aat 243
Ser Pro Asp Pro Glu Asn Ser Phe Glu Met Gln Lys Gly Asp Gln Asn
      45          50           55

cct caa att gcg gca cat gtc ata agt gag gcc agc agt aaa aca aca 291
Pro Gln Ile Ala Ala His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr
      60          65           70

tct gtg tta cag tgg gct gaa aaa gga tac tac acc atg agc aac aac 339
Ser Val Leu Gln Trp Ala Glu Lys Gly Tyr Tyr Met Ser Asn Asn
      75          80           85

ttg gta acc ctg gaa aat ggg aaa cag ctg acc gtt aaa aga caa gga 387
Leu Val Thr Leu Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly
      90          95           100          105

ctc tat tat atc tat gcc caa gtc acc ttc tgt tcc aat cgg gaa gct 435
Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala
      110         115          120

tcg agt caa gct cca ttt ata gcc agc ctc tgc cta aag tcc ccc ggt 483
Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly
      125         130          135

aga ttc gag aga atc tta ctc aga gct gca aat acc cac agt tcc gcc 531
Arg Phe Glu Arg Ile Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala
      140         145          150

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aaa cct tgc ggg caa caa tcc att cac ttg gga gga gta ttt gaa ttg	579		
Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu			
155	160	165	
caa cca ggt gct tcg gtg ttt gtc aat gtg act gat cca agc caa gtg	627		
Gln Pro Gly Ala Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val			
170	175	180	185
agc cat ggc act ggc ttc acg tcc ttt ggc tta ctc aaa ctc gag	672		
Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu Glu			
190	195	200	
tgataatcta ga			684

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<210> 20
<211> 742
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      HIV-human fusion construct

<220>
<221> SIGNAL
<222> (1)..(20)
<223> Synthetic secretory signal peptide

<220>
<221> DOMAIN
<222> (21)..(526)
<223> HIV gp120 domain with (Gly4Ser)3 linker

<220>
<221> BINDING
<222> (529)..(742)
<223> CD154 extracellular domain long form amino acids 48(Arg) to
      261(Leu) + Glu binds CD40

<400> 20
Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe Trp Ile Ser
-20           -15            -10             -5
                  15              20              25

Ala Ser Arg Ser Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr
-1     1           5           10

Glu Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Arg Glu
15          20           25

Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr
30          35           40

Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro
45          50           55           60

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Asn	Pro	Gln	Glu	Val	Val	Leu	Gly	Asn	Val	Thr	Glu	Asn	Phe	Asn	Met
				65					70						75
Trp	Lys	Asn	Asn	Met	Val	Asp	Gln	Met	His	Glu	Asp	Ile	Ile	Ser	Leu
				80				85							90
Trp	Asp	Glu	Ser	Leu	Lys	Pro	Cys	Val	Lys	Leu	Thr	Pro	Leu	Cys	Val
				95				100							105
Thr	Leu	Asn	Cys	Thr	Asn	Leu	Asn	Ile	Thr	Lys	Asn	Thr	Thr	Asn	Pro
				110				115							120
Thr	Ser	Ser	Ser	Trp	Gly	Met	Met	Glu	Lys	Gly	Glu	Ile	Lys	Asn	Cys
				125			130		135						140
Ser	Phe	Tyr	Ile	Thr	Thr	Ser	Ile	Arg	Asn	Lys	Val	Lys	Glu	Tyr	
				145				150							155
Ala	Leu	Phe	Asn	Arg	Leu	Asp	Val	Val	Pro	Ile	Glu	Asn	Thr	Asn	Asn
				160				165							170
Thr	Lys	Tyr	Arg	Leu	Ile	Ser	Cys	Asn	Thr	Ser	Val	Ile	Thr	Gln	Ala
				175			180								185
Cys	Pro	Lys	Val	Ser	Phe	Gln	Pro	Ile	Pro	Ile	His	Tyr	Cys	Val	Pro
				190			195				200				
Ala	Gly	Phe	Ala	Met	Leu	Lys	Cys	Asn	Asn	Lys	Thr	Phe	Asn	Gly	Ser
				205			210			215					220
Gly	Pro	Cys	Thr	Asn	Val	Ser	Thr	Val	Gln	Cys	Thr	His	Gly	Ile	Arg
				225			230								235
Pro	Val	Val	Ser	Thr	Gln	Leu	Leu	Leu	Asn	Gly	Ser	Leu	Ala	Glu	Glu
				240				245							250
Asp	Ile	Val	Ile	Arg	Ser	Glu	Asn	Phe	Thr	Asp	Asn	Ala	Lys	Thr	Ile
				255			260								265
Ile	Val	Gln	Leu	Asn	Glu	Ser	Val	Val	Ile	Asn	Cys	Thr	Arg	Pro	Asn
				270			275				280				
Asn	Asn	Thr	Arg	Arg	Arg	Leu	Ser	Ile	Gly	Pro	Gly	Arg	Ala	Phe	Tyr
				285			290			295					300
Ala	Arg	Arg	Asn	Ile	Ile	Gly	Asp	Ile	Arg	Gln	Ala	His	Cys	Asn	Ile
				305				310							315
Ser	Arg	Ala	Lys	Trp	Asn	Asn	Thr	Leu	Gln	Gln	Ile	Val	Ile	Lys	Leu
				320				325							330
Arg	Glu	Lys	Phe	Arg	Asn	Lys	Thr	Ile	Ala	Phe	Asn	Gln	Ser	Ser	Gly
				335			340				345				
Gly	Asp	Pro	Glu	Ile	Val	Met	His	Ser	Phe	Asn	Cys	Gly	Gly	Glu	Phe
				350			355				360				

Phe Tyr Cys Asn Thr Ala Gln Leu Phe Asn Ser Thr Trp Asn Val Thr
 365 370 375 380

 Gly Gly Thr Asn Gly Thr Glu Gly Asn Asp Ile Ile Thr Leu Gln Cys
 385 390 395

 Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Lys Val Gly Lys Ala Met
 400 405 410

 Tyr Ala Pro Pro Ile Thr Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr
 415 420 425

 Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Thr Glu Thr Glu Thr
 430 435 440

 Glu Ile Phe Arg Pro Gly Gly Asp Met Arg Asp Asn Trp Arg Ser
 445 450 455 460

 Glu Leu Tyr Lys Tyr Lys Val Val Arg Ile Glu Pro Ile Gly Val Ala
 465 470 475

 Pro Thr Arg Ala Lys Arg Arg Thr Val Gln Arg Glu Lys Arg Gly Gly
 480 485 490

 Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Asp Pro Arg
 495 500 505

 Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val
 510 515 520

 Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser
 525 530 535 540

 Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys
 545 550 555

 Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu
 560 565 570

 Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser
 575 580 585

 Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly
 590 595 600

 Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln
 605 610 615 620

 Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr
 625 630 635

 Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser
 640 645 650

 Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala
 655 660 665

Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His
 670 675 680

Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn
 685 690 695 700

Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe
 705 710 715

Gly Leu Leu Lys Leu Glu
 720

<210> 21

<211> 728

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 HIV-human fusion construct

<220>

<221> SIGNAL

<222> (1)..(20)

<223> Synthetic secretory signal peptide

<220>

<221> DOMAIN

<222> (21)..(513)

<223> HIV gp120 domain with ProAspPro linker

<220>

<221> BINDING

<222> (514)..(728)

<223> CD154 extracellular domain long form amino acids 48(Arg) to
 261(Leu) + Glu binds CD40

<400> 21

Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe Trp Ile Ser
 -20 -15 -10 -5

Ala Ser Arg Ser Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr
 -1 1 5 10

Glu Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Arg Glu
 15 20 25

Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr
 30 35 40

Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro
 45 50 55 60

Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Asn Phe Asn Met
 65 70 75

Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile Ser Leu
 80 85 90

Trp Asp Glu Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val
 95 100 105

Thr Leu Asn Cys Thr Asn Leu Asn Ile Thr Lys Asn Thr Thr Asn Pro
 110 115 120

Thr Ser Ser Ser Trp Gly Met Met Glu Lys Gly Glu Ile Lys Asn Cys
 125 130 135 140

Ser Phe Tyr Ile Thr Thr Ser Ile Arg Asn Lys Val Lys Lys Glu Tyr
 145 150 155

Ala Leu Phe Asn Arg Leu Asp Val Val Pro Ile Glu Asn Thr Asn Asn
 160 165 170

Thr Lys Tyr Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala
 175 180 185

Cys Pro Lys Val Ser Phe Gln Pro Ile Pro Ile His Tyr Cys Val Pro
 190 195 200

Ala Gly Phe Ala Met Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Ser
 205 210 215 220

Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg
 225 230 235

Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu
 240 245 250

Asp Ile Val Ile Arg Ser Glu Asn Phe Thr Asp Asn Ala Lys Thr Ile
 255 260 265

Ile Val Gln Leu Asn Glu Ser Val Val Ile Asn Cys Thr Arg Pro Asn
 270 275 280

Asn Asn Thr Arg Arg Arg Leu Ser Ile Gly Pro Gly Arg Ala Phe Tyr
 285 290 295 300

Ala Arg Arg Asn Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile
 305 310 315

Ser Arg Ala Lys Trp Asn Asn Thr Leu Gln Gln Ile Val Ile Lys Leu
 320 325 330

Arg Glu Lys Phe Arg Asn Lys Thr Ile Ala Phe Asn Gln Ser Ser Gly
 335 340 345

Gly Asp Pro Glu Ile Val Met His Ser Phe Asn Cys Gly Gly Glu Phe
 350 355 360

Phe Tyr Cys Asn Thr Ala Gln Leu Phe Asn Ser Thr Trp Asn Val Thr
 365 370 375 380

Gly Gly Thr Asn Gly Thr Glu Gly Asn Asp Ile Ile Thr Leu Gln Cys
 385 390 395
 Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Lys Val Gly Lys Ala Met
 400 405 410
 Tyr Ala Pro Pro Ile Thr Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr
 415 420 425
 Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Thr Glu Thr Glu Thr
 430 435 440
 Glu Ile Phe Arg Pro Gly Gly Asp Met Arg Asp Asn Trp Arg Ser
 445 450 455 460
 Glu Leu Tyr Lys Tyr Lys Val Val Arg Ile Glu Pro Ile Gly Val Ala
 465 470 475
 Pro Thr Arg Ala Lys Arg Arg Thr Val Gln Arg Glu Lys Arg Pro Asp
 480 485 490
 Pro Arg Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp
 495 500 505
 Phe Val Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser
 510 515 520
 Leu Ser Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe
 525 530 535 540
 Val Lys Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser
 545 550 555
 Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val
 560 565 570
 Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu
 575 580 585
 Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly
 590 595 600
 Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln
 605 610 615 620
 Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile
 625 630 635
 Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu
 640 645 650
 Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser
 655 660 665
 Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe
 670 675 680

Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr
 685 690 695 700

Ser Phe Gly Leu Leu Lys Leu Glu
 705

<210> 22

<211> 682

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 HIV-human fusion construct

<220>

<221> SIGNAL

<222> (1)..(20)

<223> Synthetic secretory signal peptide

<220>

<221> DOMAIN

<222> (21)..(525)

<223> HIV gp120 domain with (Gly4Ser)3 linker

<220>

<221> BINDING

<222> (528)..(682)

<223> CD154 extracellular domain long form amino acids 108(Glu) to
 261(Leu) + Glu binds CD40

<400> 22

Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe Trp Ile Ser
 -20 -15 -10 -5

Ala Ser Arg Ser Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr
 -1 1 5 10

Glu Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Arg Glu
 15 20 25

Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr
 30 35 40

Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro
 45 50 55 60

Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Asn Phe Asn Met
 65 70 75

Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile Ser Leu
 80 85 90

Trp Asp Glu Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val
 95 100 105

Thr Leu Asn Cys Thr Asn Leu Asn Ile Thr Lys Asn Thr Thr Asn Pro
 110 115 120

Thr Ser Ser Ser Trp Gly Met Met Glu Lys Gly Glu Ile Lys Asn Cys
 125 130 135 140

Ser Phe Tyr Ile Thr Thr Ser Ile Arg Asn Lys Val Lys Lys Glu Tyr
 145 150 155

Ala Leu Phe Asn Arg Leu Asp Val Val Pro Ile Glu Asn Thr Asn Asn
 160 165 170

Thr Lys Tyr Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala
 175 180 185

Cys Pro Lys Val Ser Phe Gln Pro Ile Pro Ile His Tyr Cys Val Pro
 190 195 200

Ala Gly Phe Ala Met Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Ser
 205 210 215 220

Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg
 225 230 235

Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu
 240 245 250

Asp Ile Val Ile Arg Ser Glu Asn Phe Thr Asp Asn Ala Lys Thr Ile
 255 260 265

Ile Val Gln Leu Asn Glu Ser Val Val Ile Asn Cys Thr Arg Pro Asn
 270 275 280

Asn Asn Thr Arg Arg Arg Leu Ser Ile Gly Pro Gly Arg Ala Phe Tyr
 285 290 295 300

Ala Arg Arg Asn Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile
 305 310 315

Ser Arg Ala Lys Trp Asn Asn Thr Leu Gln Gln Ile Val Ile Lys Leu
 320 325 330

Arg Glu Lys Phe Arg Asn Lys Thr Ile Ala Phe Asn Gln Ser Ser Gly
 335 340 345

Gly Asp Pro Glu Ile Val Met His Ser Phe Asn Cys Gly Gly Glu Phe
 350 355 360

Phe Tyr Cys Asn Thr Ala Gln Leu Phe Asn Ser Thr Trp Asn Val Thr
 365 370 375 380

Gly Gly Thr Asn Gly Thr Glu Gly Asn Asp Ile Ile Thr Leu Gln Cys
 385 390 395

Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Lys Val Gly Lys Ala Met
 400 405 410
 Tyr Ala Pro Pro Ile Thr Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr
 415 420 425
 Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Thr Glu Thr Glu Thr
 430 435 440
 Glu Ile Phe Arg Pro Gly Gly Asp Met Arg Asp Asn Trp Arg Ser
 445 450 455 460
 Glu Leu Tyr Lys Tyr Lys Val Val Arg Ile Glu Pro Ile Gly Val Ala
 465 470 475
 Pro Thr Arg Ala Lys Arg Arg Thr Val Gln Arg Glu Lys Arg Gly Gly
 480 485 490
 Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Asp Pro Glu
 495 500 505
 Asn Ser Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala
 510 515 520
 His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp
 525 530 535 540
 Ala Glu Lys Gly Tyr Tyr Met Ser Asn Asn Leu Val Thr Leu Glu
 545 550 555
 Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr
 560 565 570
 Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro
 575 580 585
 Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile
 590 595 600
 Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln
 605 610 615 620
 Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser
 625 630 635
 Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly
 640 645 650
 Phe Thr Ser Phe Gly Leu Leu Lys Leu Glu
 655 660

<210> 23
 <211> 668
 <212> PRT
 <213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
      HIV-human fusion construct

<220>
<221> SIGNAL
<222> (1)..(20)
<223> Synthetic secretory signal peptide

<220>
<221> DOMAIN
<222> (21)..(513)
<223> HIV gp120 domain with ProAspPro linker

<220>
<221> BINDING
<222> (514)..(668)
<223> CD154 extracellular domain long form amino acids 108(Glu) to
      261(Leu) + Glu binds CD40

<400> 23
Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe Trp Ile Ser
-20           -15           -10           -5

Ala Ser Arg Ser Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr
-1   1           5           10

Glu Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Arg Glu
15           20           25

Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr
30           35           40

Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro
45           50           55           60

Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Asn Phe Asn Met
65           70           75

Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile Ser Leu
80           85           90

Trp Asp Glu Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val
95           100          105

Thr Leu Asn Cys Thr Asn Leu Asn Ile Thr Lys Asn Thr Thr Asn Pro
110          115          120

Thr Ser Ser Ser Trp Gly Met Met Glu Lys Gly Glu Ile Lys Asn Cys
125          130          135          140

Ser Phe Tyr Ile Thr Thr Ser Ile Arg Asn Lys Val Lys Lys Glu Tyr
145          150          155

Ala Leu Phe Asn Arg Leu Asp Val Val Pro Ile Glu Asn Thr Asn Asn
160          165          170

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Thr Lys Tyr Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala
 175 180 185
 Cys Pro Lys Val Ser Phe Gln Pro Ile Pro Ile His Tyr Cys Val Pro
 190 195 200
 Ala Gly Phe Ala Met Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Ser
 205 210 215 220
 Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg
 225 230 235
 Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu
 240 245 250
 Asp Ile Val Ile Arg Ser Glu Asn Phe Thr Asp Asn Ala Lys Thr Ile
 255 260 265
 Ile Val Gln Leu Asn Glu Ser Val Val Ile Asn Cys Thr Arg Pro Asn
 270 275 280
 Asn Asn Thr Arg Arg Arg Leu Ser Ile Gly Pro Gly Arg Ala Phe Tyr
 285 290 295 300
 Ala Arg Arg Asn Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile
 305 310 315
 Ser Arg Ala Lys Trp Asn Asn Thr Leu Gln Gln Ile Val Ile Lys Leu
 320 325 330
 Arg Glu Lys Phe Arg Asn Lys Thr Ile Ala Phe Asn Gln Ser Ser Gly
 335 340 345
 Gly Asp Pro Glu Ile Val Met His Ser Phe Asn Cys Gly Gly Glu Phe
 350 355 360
 Phe Tyr Cys Asn Thr Ala Gln Leu Phe Asn Ser Thr Trp Asn Val Thr
 365 370 375 380
 Gly Gly Thr Asn Gly Thr Glu Gly Asn Asp Ile Ile Thr Leu Gln Cys
 385 390 395
 Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Lys Val Gly Lys Ala Met
 400 405 410
 Tyr Ala Pro Pro Ile Thr Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr
 415 420 425
 Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Thr Glu Thr Glu Thr
 430 435 440
 Glu Ile Phe Arg Pro Gly Gly Asp Met Arg Asp Asn Trp Arg Ser
 445 450 455 460
 Glu Leu Tyr Lys Tyr Lys Val Val Arg Ile Glu Pro Ile Gly Val Ala
 465 470 475

Pro Thr Arg Ala Lys Arg Arg Thr Val Gln Arg Glu Lys Arg Pro Asp
 480 485 490

Pro Glu Asn Ser Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile
 495 500 505

Ala Ala His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu
 510 515 520

Gln Trp Ala Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr
 525 530 535 540

Leu Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr
 545 550 555

Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln
 560 565 570

Ala Pro Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu
 575 580 585

Arg Ile Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys
 590 595 600

Gly Gln Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly
 605 610 615 620

Ala Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly
 625 630 635

Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu Glu
 640 645

<210> 24
 <211> 294
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 HIV-human fusion construct

<220>
 <221> SIGNAL
 <222> (1)..(20)
 <223> Synthetic secretory signal peptide

<220>
 <221> DOMAIN
 <222> (21)..(77)
 <223> HIV gp120 V3 loop with (Gly4Ser)3 linker

<220>
 <221> BINDING
 <222> (80)...(294)
 <223> CD154 extracellular domain long form amino acids 48(Arg) to
 261(Leu) + Glu binds CD40

<400> 24
 Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe Trp Ile Ser
 -20 -15 -10 -5

Ala Ser Arg Ser Val Val Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr
 -1 1 5 10

Arg Arg Arg Leu Ser Ile Gly Pro Gly Arg Ala Phe Tyr Ala Arg Arg
 15 20 25

Asn Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile Ser Gly Gly
 30 35 40

Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Asp Pro Arg
 45 50 55 60

Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val
 65 70 75

Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser
 80 85 90

Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys
 95 100 105

Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu
 110 115 120

Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser
 125 130 135 140

Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly
 145 150 155

Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln
 160 165 170

Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr
 175 180 185

Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser
 190 195 200

Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala
 205 210 215 220

Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His
 225 230 235

Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn
 240 245 250

Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe
255 260 265
Gly Leu Leu Lys Leu Glu
270

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<210> 25
<211> 280
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      HIV-human fusion construct

<220>
<221> SIGNAL
<222> (1)..(20)
<223> Synthetic secretory signal peptide

<220>
<221> DOMAIN
<222> (21)..(65)
<223> HIV gp120 V3 loop with ProAspPro linker

<220>
<221> BINDING
<222> (66)..(280)
<223> CD154 extracellular domain long form amino acids 48(Arg) to
      261(Leu) + Glu binds CD40

<400> 25
Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe Trp Ile Ser
-20           -15                   -10                   -5

Ala Ser Arg Ser Val Val Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr
-1   1           5                   10

Arg Arg Arg Leu Ser Ile Gly Pro Gly Arg Ala Phe Tyr Ala Arg Arg
15          20                   25

Asn Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile Ser Pro Asp
30          35                   40

Pro Arg Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp
45          50                   55                   60

Phe Val Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser
65          70                   .                   75

Leu Ser Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe
80          85                   90

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Val	Lys	Asp	Ile	Met	Leu	Asn	Lys	Glu	Glu	Thr	Lys	Lys	Glu	Asn	Ser
95							100					105			
Phe	Glu	Met	Gln	Lys	Gly	Asp	Gln	Asn	Pro	Gln	Ile	Ala	Ala	His	Val
110						115					120				
Ile	Ser	Glu	Ala	Ser	Ser	Lys	Thr	Thr	Ser	Val	Leu	Gln	Trp	Ala	Glu
125					130					135			140		
Lys	Gly	Tyr	Tyr	Thr	Met	Ser	Asn	Asn	Leu	Val	Thr	Leu	Glu	Asn	Gly
					145				150			155			
Lys	Gln	Leu	Thr	Val	Lys	Arg	Gln	Gly	Leu	Tyr	Tyr	Ile	Tyr	Ala	Gln
				160					165			170			
Val	Thr	Phe	Cys	Ser	Asn	Arg	Glu	Ala	Ser	Ser	Gln	Ala	Pro	Phe	Ile
					175				180			185			
Ala	Ser	Leu	Cys	Leu	Lys	Ser	Pro	Gly	Arg	Phe	Glu	Arg	Ile	Leu	Leu
					190			195			200				
Arg	Ala	Ala	Asn	Thr	His	Ser	Ser	Ala	Lys	Pro	Cys	Gly	Gln	Gln	Ser
					205		210			215			220		
Ile	His	Leu	Gly	Gly	Val	Phe	Glu	Leu	Gln	Pro	Gly	Ala	Ser	Val	Phe
					225			230			235				
Val	Asn	Val	Thr	Asp	Pro	Ser	Gln	Val	Ser	His	Gly	Thr	Gly	Phe	Thr
					240			245			250				
Ser	Phe	Gly	Leu	Leu	Lys	Leu	Glu								
					255		260								

<210> 26
<211> 234
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
HIV-human fusion construct

<220>
<221> SIGNAL
<222> (1)..(20)
<223> Synthetic secretory signal peptide

<220>
<221> DOMAIN
<222> (21)..(77)
<223> HIV gp120 V3 loop with (Gly4Ser)3 linker

<220>
<221> BINDING

<222> (80)..(234)
 <223> CD154 extracellular domain long form amino acids 108(Glu) to
 261(Leu) + Glu binds CD40

<400> 26
 Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Phe Trp Ile Ser
 -20 -15 -10 -5

Ala Ser Arg Ser Val Val Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr
 -1 1 5 10

Arg Arg Arg Leu Ser Ile Gly Pro Gly Arg Ala Phe Tyr Ala Arg Arg
 15 20 25

Asn Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile Ser Gly Gly
 30 35 40

Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Asp Pro Glu
 45 50 55 60

Asn Ser Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala
 65 70 75

His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp
 80 85 90

Ala Glu Lys Gly Tyr Tyr Met Ser Asn Asn Leu Val Thr Leu Glu
 95 100 105

Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr
 110 115 120

Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro
 125 130 135 140

Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile
 145 150 155

Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln
 160 165 170

Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser
 175 180 185

Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly
 190 195 200

Phe Thr Ser Phe Gly Leu Leu Lys Leu Glu
 205 210

<210> 27
 <211> 220
 <212> PRT
 <213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
      HIV-human fusion construct

<220>
<221> SIGNAL
<222> (1)..(20)
<223> Synthetic secretory signal peptide

<220>
<221> DOMAIN
<222> (21)..(65)
<223> HIV gp120 V3 loop with ProAspPro linker

<220>
<221> BINDING
<222> (66)..(220)
<223> CD154 extracellular domain long form amino acids 108(Glu) to
      261(Leu) + Glu binds CD40

<400> 27
Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe Trp Ile Ser
-20           -15           -10           -5

Ala Ser Arg Ser Val Val Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr
-1   1           5           10

Arg Arg Arg Leu Ser Ile Gly Pro Gly Arg Ala Phe Tyr Ala Arg Arg
15           20           25

Asn Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile Ser Pro Asp
30           35           40

Pro Glu Asn Ser Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile
45           50           55           60

Ala Ala His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu
65           70           75

Gln Trp Ala Glu Lys Gly Tyr Tyr Met Ser Asn Asn Leu Val Thr
80           85           90

Leu Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr
95           100          105

Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln
110          115          120

Ala Pro Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu
125          130          135          140

Arg Ile Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys
145          150          155

Gly Gln Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly
160          165          170

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Ala Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly
175 180 185

Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu Glu
190 195 200

<210> 28

<211> 6

<212> PRT

<213> Human immunodeficiency virus type 1

<400> 28

Gly Pro Gly Arg Ala Phe
1 5

<210> 29

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Linker peptide

<400> 29

Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10 15